In the claims:

Claim 1 (Canceled)

Claims 2–6 (Withdrawn)

Claim 7 (Canceled)

Claims 8-13 (Withdrawn)

Claim 14. (New): A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in a P2X7 gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as having or at risk for having a P2X7-mediated disease, wherein the sample comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2; and

(b) testing the sample to determine the identity of the nucleotide.

Claim 15 (New): The method of claim 14, wherein the nucleic acid sample comprises a fragment of a P2X7 DNA.

Claim 16 (New): The method of claim 14, wherein the human is diagnosed as having, or at risk for having, hyperlipoproteinemia, cardiovascular disease, rheumatoid arthritis, osteoarthritis, psoriasis, allergic dermatitis, asthma, chronic obstructive pulmonary disease (COPD), hyperresponsiveness of the airway, septic shock, glomerulonephritis, irritable bowel disease, Crohn's disease, ulcerative colitis, atherosclerosis, growth and metastases of malignant cells, myoblastic leukemia, diabetes, Alzheimer's disease, meningitis, osteoporosis, a burn injury, ischaemic heart disease, stroke, or vericose veins.

Claim 17 (New): The method of claim 14, wherein step (b) comprises performing an ARMS™ assay or RFLP.

Claim 18 (New): The method of claim 14, further comprising:

(c) determining that the nucleotide at position 1513 of SEQ ID NO:2 is a C.

Claim 19 (New): The method of claim 14, further comprising:

(c) determining that the nucleotide at position 1513 of SEQ ID NO:2 is not an A.

Claim 20 (New): A method for determining the presence or absence of a SNP in a P2X7 gene, the method comprising:

(a) providing a nucleic acid sample from a human, wherein the sample comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2; and

(b) determining the identity of the nucleotide by using a technique selected from the group consisting of the ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, or a restriction site-based PCR or FRET technique.

Claim 21 (New): The method of claim 20, wherein the nucleic acid sample comprises a fragment of a P2X7 DNA.

Claim 22 (New): A method for determining the presence or absence of a SNP in a P2X7 gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as having, or at risk for having, hyperlipoproteinemia, cardiovascular disease, rheumatoid arthritis, osteoarthritis, psoriasis, allergic dermatitis, asthma, chronic obstructive pulmonary disease (COPD), hyperresponsiveness of the airway, septic shock, glomerulonephritis, irritable bowel disease, Crohn's disease, ulcerative colitis, atherosclerosis, growth and metastases of malignant cells, myoblastic leukemia, diabetes, Alzheimer's disease, meningitis, osteoporosis, a burn injury, ischaemic heart disease, stroke, or vericose veins, wherein the sample comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2, and

(b) testing the sample to determine the identity of the nucleotide by using a technique selected from the group consisting of the ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, or a restriction site-based PCR or FRET technique.

Claim 23 (New): A method for determining the presence or absence of a SNP in a P2X7 gene in a nucleic acid sample of a human, the method comprising determining that the nucleotide in the sample corresponding to position 1513 of SEQ ID NO:2 is a C.

Claim 24 (New): A method for determining the presence or absence of a SNP in a P2X7 gene in a nucleic acid sample of a human, the method comprising determining that the nucleotide in the sample corresponding to position 1513 of SEQ ID NO:2 is not an A.

Claim 25 (New): A method for characterizing the genotype of a human diagnosed as having a P2X7-mediated disease or as being at risk for having a P2X7-mediated disease, the method comprising:

(a) providing a nucleic acid sample from the human, wherein the sample comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2;

(b) testing the sample to determine the identity of the nucleotide; and

(c) recording the identity of the nucleotide in a print or computer-readable medium.

Claim 26 (New): A method for characterizing the genotype of a human diagnosed as having, or at risk for having, hyperlipoproteinemia, cardiovascular disease, rheumatoid arthritis, osteoarthritis, psoriasis, allergic dermatitis, asthma, chronic obstructive pulmonary disease (COPD), hyperresponsiveness of the airway, septic shock, glomerulonephritis, irritable bowel disease, Crohn's disease, ulcerative colitis, atherosclerosis, growth and metastases of malignant cells, myoblastic leukemia, diabetes, Alzheimer's disease, meningitis, osteoporosis, a burn injury, ischaemic heart disease, stroke, or vericose veins, the method comprising:

(a) providing a nucleic acid sample from the human, wherein the sample comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2;

(b) testing the sample to determine the identity of the nucleotide; and

(c) recording the identity of the nucleotide in a print or computer-readable medium.

Claim 27 (New): A method of performing a linkage study, the method comprising:

a) providing a nucleic acid sample from each of two or more individuals having or at risk for having a P2X7-mediated disease, wherein the sample comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2;

b) testing each sample to determine the identity of the nucleotide; and

c) correlating (i) the frequency with which a C occurs at the position corresponding to position 1513 of SEQ ID NO:2 in the samples, with (ii) the frequency with which C occurs at the position corresponding to position 1513 of SEQ ID NO:2 in nucleic acid samples from the population at large.

Claim 28 (New): A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in a P2X7 gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as having or at risk for having a P2X7-mediated disease, wherein the sample comprises a nucleotide at each of the following nucleotide positions:

positions 936, 1012, 1147, 1343 and 1476 in the 5′ UTR region of the P2X7 gene as defined by the positions in SEQ ID NO: 1;

positions 253, 488, 489, 760, 835, 853, 1068, 1096, 1315, 1324, 1405, 1448, 1494, 1513, 1628 and 1772 in the coding region of the P2X7 gene as defined by the positions in SEQ ID NO: 2; and

positions 4780, 4845, 4849, 5021, 5554, 5579, 5535, 5845 and 6911 in the intron region of the P2X7 gene as defined by the positions in SEQ ID NO: 3; and

(b) testing the sample to determine the identity of all 30 nucleotides.

Claim 29 (New): A method for characterizing the genotype of a human diagnosed as having a P2X7-mediated disease, or as being at risk for having a P2X7-mediated disease, the method comprising:

(a) providing a nucleic acid sample from a human identified as having, or at risk for having, a P2X7-mediated disease, wherein the sample comprises a nucleotide at a each of the following nucleotide positions:

positions 936, 1012, 1147, 1343 and 1476 in the 5′ UTR region of the P2X7 gene as defined by the positions in SEQ ID NO: 1;

positions 253, 488, 489, 760, 835, 853, 1068, 1096, 1315, 1324, 1405, 1448, 1494, 1513, 1628 and 1772 in the coding region of the P2X7 gene as defined by the positions in SEQ ID NO: 2; and

positions 4780, 4845, 4849, 5021, 5554, 5579, 5535, 5845 and 6911 in the intron region of the P2X7 gene as defined by the positions in SEQ ID NO: 3;

(b) testing the sample to determine the identity of nucleotide at one or more of the nucleotide positions; and

(c) recording the identity of the nucleotide in a print- or machine-readable medium.

Claim 30 (New): A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in a P2X7 gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as having or at risk for having a P2X7-mediated disease, wherein the sample comprises a nucleotide at a position corresponding to position 1513 of SEQ ID NO:2 and a nucleotide at at least one more position selected from the group consisting of:

positions 936, 1012, 1147, 1343 and 1476 in the 5′ UTR region of the P2X7 gene as defined by the positions in SEQ ID NO: 1;

positions 253, 488, 489, 760, 835, 853, 1068, 1096, 1315, 1324, 1405, 1448, 1494, 1628 and 1772 in the coding region of the P2X7 gene as defined by the positions in SEQ ID NO: 2; and

positions 4780, 4845, 4849, 5021, 5554, 5579, 5535, 5845 and 6911 in the intron region of the P2X7 gene as defined by the positions in SEQ ID NO: 3; and

(b) testing the sample to determine the identity of the nucleotide at one or more of the nucleotide positions.